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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/552,705DATE: 05/08/2000  
TIME: 18:55:23

Input Set: I552705.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

1 <110> APPLICANT: Chen, Shuian  
2 Zhou, Dujin  
3 <120> TITLE OF INVENTION: DRUG SCREENING USING A PROLINE-RICH NUCLEAR RECEPTOR  
4 CO-REGULATORY PROTEIN/NUCLEAR RECEPTOR CO-EXPRESSION  
5 SYSTEM  
6 <130> FILE REFERENCE: 2124-311  
7 <140> CURRENT APPLICATION NUMBER: US/09/552,705  
8 <141> CURRENT FILING DATE: 2000-04-19  
9 <150> EARLIER APPLICATION NUMBER: U.S. 60/129,873  
10 <151> EARLIER FILING DATE: 1999-04-19  
11 <160> NUMBER OF SEQ ID NOS: 9  
12 <170> SOFTWARE: PatentIn Ver. 2.0  
13 <210> SEQ ID NO 1  
14 <211> LENGTH: 30  
15 <212> TYPE: DNA  
16 <213> ORGANISM: Artificial Sequence  
17 <220> FEATURE:  
18 <223> OTHER INFORMATION: Description of Artificial Sequence:Sense primer.  
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21 <210> SEQ ID NO 2  
22 <211> LENGTH: 39  
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24 <213> ORGANISM: Artificial Sequence  
25 <220> FEATURE:  
26 <223> OTHER INFORMATION: Description of Artificial Sequence:Antisense  
27 primer.  
28 <400> SEQUENCE: 2  
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30 <210> SEQ ID NO 3  
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33 <213> ORGANISM: Homo sapiens  
34 <400> SEQUENCE: 3  
35 ccaaggtaaa 12  
36 <210> SEQ ID NO 4  
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38 <212> TYPE: PRT  
39 <213> ORGANISM: Homo sapiens  
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41 Leu Lys Thr Leu Leu  
42 1 5  
43 <210> SEQ ID NO 5  
44 <211> LENGTH: 7

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45 <212> TYPE: PRT  
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49 1 5  
50 <210> SEQ ID NO 6  
51 <211> LENGTH: 7  
52 <212> TYPE: PRT  
53 <213> ORGANISM: Homo sapiens  
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55 <221> NAME/KEY: MUTAGEN  
56 <222> LOCATION: (3)  
57 <223> OTHER INFORMATION: This residue has been changed from a proline.  
58 <220> FEATURE:  
59 <221> NAME/KEY: MUTAGEN  
60 <222> LOCATION: (6)  
61 <223> OTHER INFORMATION: This residue has been changed from a proline.  
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64 1 5  
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66 <211> LENGTH: 2061  
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74 ggcttcacct ttccttctc tcttcgttgc tgagcgacaa gcttccttagc gct atg 116  
75 Met  
76 1  
77 act gtc gtc tcc gtc ccg cag cggttccgatc gtc ctg ggt ggc cgc 164  
78 Thr Val Val Ser Val Pro Gln Arg Glu Pro Leu Val Leu Gly Gly Arg  
79 5 10 15  
80 ctt gcg ccg ctt ggc ttt tcc tcc cga ggt tac ttt ggg gcc ctc ccg 212  
81 Leu Ala Pro Leu Gly Phe Ser Ser Arg Gly Tyr Phe Gly Ala Leu Pro  
82 20 25 30  
83 atg gtg acc acg gct ccg cct cct tta ccc ccg atc ccg gac ccc ccg 260  
84 Met Val Thr Ala Pro Pro Leu Pro Arg Ile Pro Asp Pro Arg  
85 35 40 45  
86 gca ctg ccc ccg acc ctc ttc ctc cct cat ttc cta ggg gga gat ggc 308  
87 Ala Leu Pro Pro Thr Leu Phe Leu Pro His Phe Leu Gly Gly Asp Gly  
88 50 55 60 65  
89 ccg tgt ctg acc ccc cag cct cgc gct cca gca gct ctg ccc aac cgc 356  
90 Pro Cys Leu Thr Pro Gln Pro Arg Ala Pro Ala Ala Leu Pro Asn Arg  
91 70 75 80  
92 agc ctc gcc gtg gcg gga ggc act cct ccg gca gcg ccg aag aag ccg 404  
93 Ser Leu Ala Val Ala Gly Gly Thr Pro Arg Ala Ala Pro Lys Lys Arg  
94 85 90 95

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95	cga aag aag aag gtg cg	cc	gca ggg cag ctg ccc agc cgc	452
96	Arg Lys Lys Lys Val Arg Ala Ser Pro Ala Gly Gln Leu Pro Ser Arg			
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98	ttc cac cag tac cag cag cac cg	gg	gtc ccc ggc ggc cgg agc	500
99	Phe His Gln Tyr Gln Gln His Arg Pro Ser Leu Glu Gly Gly Arg Ser			
100	115	120	125	
101	ccc gcg acc ggc ccg agc gga gc	g	gag gtc ccc ggc ggc ccc gcc	548
102	Pro Ala Thr Gly Pro Ser Gly Ala Gln Glu Val Pro Gly Pro Ala Ala			
103	130	135	140	145
104	gcc ttg gcc ccg agt cct gca gca gc	g	gcg gag gga gcc agc	596
105	Ala Leu Ala Pro Ser Pro Ala Ala Ala Gly Thr Glu Gly Ala Ser			
106	150	155	160	
107	ccc gac ctt gcc ccg ctg cgg ccc gc	g	ctc ccc gac acc ccc ctc	644
108	Pro Asp Leu Ala Pro Leu Arg Pro Ala Ala Pro Gly Gln Thr Pro Leu			
109	165	170	175	
110	agg aaa gag gtt tta aaa tca aag atg gga aaa tcg gag aaa att gcc			692
111	Arg Lys Glu Val Leu Lys Ser Lys Met Gly Lys Ser Glu Lys Ile Ala			
112	180	185	190	
113	ctt ccc cat ggc cag ctt gtt cat ggt ata cac ttg tat gag caa cca			740
114	Leu Pro His Gly Gln Leu Val His Gly Ile His Leu Tyr Glu Gln Pro			
115	195	200	205	
116	aag ata aac aga cag aaa agc aaa tat aac ttg cca cta acc aag atc			788
117	Lys Ile Asn Arg Gln Lys Ser Lys Tyr Asn Leu Pro Leu Thr Lys Ile			
118	210	215	220	225
119	acc tct gca aaa aga aat gaa aac aac ttg tgg cag gat tct gtt tca			836
120	Thr Ser Ala Lys Arg Asn Glu Asn Asn Phe Trp Gln Asp Ser Val Ser			
121	230	235	240	
122	tct gac aga att cag aag cag gaa aaa aag cct tt	ttt	aaa aat acc gag	884
123	Ser Asp Arg Ile Gln Lys Gln Glu Lys Lys Pro Phe Lys Asn Thr Glu			
124	245	250	255	
125	aac att aaa aat tcg cat ttg aag aaa tca gca tt	ttt	cta act gaa gtg	932
126	Asn Ile Lys Asn Ser His Leu Lys Ser Ala Phe Leu Thr Glu Val			
127	260	265	270	
128	agc caa aag gaa aat tat gct ggg gca aag tt	ttt	agt gat cca cct tct	980
129	Ser Gln Lys Glu Asn Tyr Ala Gly Ala Lys Phe Ser Asp Pro Pro Ser			
130	275	280	285	
131	cct agt gtt ctt cca aag cct cct agt cac ttg atg gga agc act gtt			1028
132	Pro Ser Val Leu Pro Lys Pro Pro Ser His Trp Met Gly Ser Thr Val			
133	290	295	300	305
134	gaa aat tcc aac caa aac agg gag ctg atg gca gta cac tta aaa acc			1076
135	Glu Asn Ser Asn Gln Asn Arg Glu Leu Met Ala Val His Leu Lys Thr			
136	310	315	320	
137	ctc ctc aaa gtt caa act tagatttcag atttcagttat gtgtgtaaaa			1124
138	Leu Leu Lys Val Gln Thr			
139	325			
140	cataatttt cccatatccc tggactcttgg agaaaaatgg tacagaaatgg gaaatggcc			1184
141	ttgttgcaac atacaattgc aaaagatgag tttaaaaaat tacataaaaa cagcttgtat			1244
142	tatattttat attttgcataa tactgtatac catgtattat gtgtatatttgcataacttgc			1304
143	agaggtatata tagattttttgcataa ttatggaaatgttgcataatgc cccatggcattgcaggttgc			1364
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 146 atctaaatgt gaacagttt ctaatgcact actgaagtt aaatctgtgg cacaatcaat 1544  
 147 gtaagcatgg ggTTTttt tctaaattga tttgtaatct gaaattactg aacaactcct 1604  
 148 attcccattt ttgctaaact caattctgg ttttggata tatccattcc agcttaatgc 1664  
 149 ctctaatttt aatgccaaca aaattgggtg taatcaaatt ttaaaataat aataattgg 1724  
 150 ccccccttt taaaatagtc ttgactctt gtgtgtgact gtttctcatg tttgaatgtg 1784  
 151 tgacttaggag atgattttgt gtgggtggat tttttgact tctactttac tggctgagtg 1844  
 152 tgagccgcca tgcctggcca taatctacat tttcttacca ggagcagcat tgagggttt 1904  
 153 gagcatagta cttgactact ctagaggctg agacgggagc atcttttag cctgagaagt 1964  
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 158 <212> TYPE: PRT  
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 164 20 25 30  
 165 Pro Met Val Thr Thr Ala Pro Pro Pro Leu Pro Arg Ile Pro Asp Pro  
 166 35 40 45  
 167 Arg Ala Leu Pro Pro Thr Leu Phe Leu Pro His Phe Leu Gly Gly Asp  
 168 50 55 60  
 169 Gly Pro Cys Leu Thr Pro Gln Pro Arg Ala Pro Ala Ala Leu Pro Asn  
 170 65 70 75 80  
 171 Arg Ser Leu Ala Val Ala Gly Gly Thr Pro Arg Ala Ala Pro Lys Lys  
 172 85 90 95  
 173 Arg Arg Lys Lys Lys Val Arg Ala Ser Pro Ala Gly Gln Leu Pro Ser  
 174 100 105 110  
 175 Arg Phe His Gln Tyr Gln Gln His Arg Pro Ser Leu Glu Gly Gly Arg  
 176 115 120 125  
 177 Ser Pro Ala Thr Gly Pro Ser Gly Ala Gln Glu Val Pro Gly Pro Ala  
 178 130 135 140  
 179 Ala Ala Leu Ala Pro Ser Pro Ala Ala Ala Gly Thr Glu Gly Ala  
 180 145 150 155 160  
 181 Ser Pro Asp Leu Ala Pro Leu Arg Pro Ala Ala Pro Gly Gln Thr Pro  
 182 165 170 175  
 183 Leu Arg Lys Glu Val Leu Lys Ser Lys Met Gly Lys Ser Glu Lys Ile  
 184 180 185 190  
 185 Ala Leu Pro His Gly Gln Leu Val His Gly Ile His Leu Tyr Glu Gln  
 186 195 200 205  
 187 Pro Lys Ile Asn Arg Gln Lys Ser Lys Tyr Asn Leu Pro Leu Thr Lys  
 188 210 215 220  
 189 Ile Thr Ser Ala Lys Arg Asn Glu Asn Asn Phe Trp Gln Asp Ser Val  
 190 225 230 235 240  
 191 Ser Ser Asp Arg Ile Gln Lys Gln Glu Lys Lys Pro Phe Lys Asn Thr  
 192 245 250 255  
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 194 260 265 270

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195 Val Ser Gln Lys Glu Asn Tyr Ala Gly Ala Lys Phe Ser Asp Pro Pro  
196 275 280 285  
197 Ser Pro Ser Val Leu Pro Lys Pro Pro Ser His Trp Met Gly Ser Thr  
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200 305 310 315 320  
201 Thr Leu Leu Lys Val Gln Thr  
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209 1 5 10 15  
210 Pro Lys Pro Pro Ser His Trp  
211 20

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VERIFICATION SUMMARY  
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Line ? Error/Warning

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